

SEQUENCE LISTING

<110> MENZEL, ROLF

<120> COMPOSITIONS AND METHODS FOR DIRECTED GENE ASSEMBLY

<130> 10424-003

<150> 60/222,134

<151> 2000-07-31

<160> 22

<170> PatentIn version 3.0

<210> 1

<211> 87

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 1

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gggcggccgc tccccgggtg gcgcgcc 87

<210> 2

<211> 87

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 2

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tggttacctt aattaagttt aaacgcg 87

<210> 3

<211> 50

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 3

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<210> 4

<211> 50

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: Primer

<400> 4
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 <210> 5
 <211> 87
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 <213> Artificial

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 <223> Description of artificial sequence: Primer

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 ggctagcgtc agctgggtac catgcat 87

 <210> 6
 <211> 87
 <212> DNA
 <213> Artificial

 <220>
 <223> Description of artificial sequence: Primer

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 tttaaaccat atgcaattgc tccatgg 87

 <210> 7
 <211> 19
 <212> DNA
 <213> Artificial

 <220>
 <223> Description of artificial sequence: Primer

 <400> 7
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 <210> 8
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <223> Description of artificial sequence: Primer

 <400> 8
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 <210> 9
 <211> 28
 <212> DNA
 <213> Artificial

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 <223> Description of artificial sequence: Primer

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ggggtaccgc ggtctattca tactttcg                                28

<210> 10
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Description of artificial sequence: Primer

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gcagatctca tttgtagaa tatggtattg agcggc                                36

<210> 11
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Description of artificial sequence: Primer

<400> 11
agcgagatct ctattattgt gcagctg                                27

<210> 12
<211> 33
<212> DNA
<213> Artificial

<220>
<223> Description of artificial sequence: Primer

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<210> 13
<211> 1140
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (1) .. (1140)

<400> 13
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Met Met Arg Lys Lys Ser Phe Trp Leu Gly Met Leu Thr Ala Leu Met
1 5 10 15
ctc gtg ttc acg atg gcc ttc agc gat tcc gcg tct gct gct cag ccg                                96
Leu Val Phe Thr Met Ala Phe Ser Asp Ser Ala Ser Ala Ala Gln Pro
20 25 30
gcg aaa aat gtt gaa aag gat tat att gtc gga ttt aag tcg gga gtg                                144
Ala Lys Asn Val Glu Lys Asp Tyr Ile Val Gly Phe Lys Ser Gly Val
35 40 45
aaa acc gca tcc gtc aaa aag gac atc atc aaa gag agc ggc gga aaa                                192
Lys Thr Ala Ser Val Lys Lys Asp Ile Ile Lys Glu Ser Gly Gly Lys
50 55 60

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gtg	gac	aag	cag	ttt	aga	atc	atc	aac	gcg	gca	aaa	gcg	aag	cta	gac	240
Val	Asp	Lys	Gln	Phe	Arg	Ile	Ile	Asn	Ala	Ala	Lys	Ala	Lys	Leu	Asp	
65				70					75					80		
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Lys	Glu	Ala	Leu	Glu	Glu	Val	Lys	Asn	Asp	Pro	Asp	Val	Ala	Tyr	Val	
				85					90					95		
gaa	gag	gat	cac	gta	gct	cat	gct	ttg	gcg	caa	acc	gtt	cct	tac	ggc	336
Glu	Glu	Asp	His	Val	Ala	His	Ala	Leu	Ala	Gln	Thr	Val	Pro	Tyr	Gly	
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Ile	Pro	Leu	Ile	Lys	Ala	Asp	Lys	Val	Gln	Ala	Gln	Gly	Tyr	Lys	Gly	
			115					120					125			
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Ala	Asn	Val	Lys	Val	Ala	Val	Leu	Asp	Thr	Gly	Ile	Gln	Ala	Ser	His	
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Pro	Asp	Leu	Asn	Val	Val	Gly	Gly	Ala	Ser	Phe	Val	Ala	Gly	Glu	Ala	
145				150									155		160	
tat	aac	acc	gac	ggc	aac	gga	cac	ggc	acg	cat	gtt	gcc	ggg	aca	gta	528
Tyr	Asn	Thr	Asp	Gly	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Thr	Val	
				165											175	
gct	gcg	ctt	gac	aat	aca	acg	ggg	gta	tta	ggc	gtt	gcg	ccg	aac	gta	576
Ala	Ala	Leu	Asp	Asn	Thr	Thr	Gly	Val	Leu	Gly	Val	Ala	Pro	Asn	Val	
				180											190	
tcc	ttg	tac	gcg	gtt	aaa	gtg	ctg	aat	tca	agc	gga	agc	gga	tct	tac	624
Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	Asn	Ser	Ser	Gly	Ser	Gly	Ser	Tyr	
				195				200						205		
agc	ggc	att	gta	agc	gga	atc	gag	tgg	gcg	acg	aca	aac	ggc	atg	gat	672
Ser	Gly	Ile	Val	Ser	Gly	Ile	Glu	Trp	Ala	Thr	Thr	Asn	Gly	Met	Asp	
				210				215					220			
gtt	atc	aac	atg	agc	ctt	gga	gga	cca	tca	ggc	tca	aca	gcg	atg	aaa	720
Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Ser	Gly	Ser	Thr	Ala	Met	Lys	
225				230									235		240	
cag	gcg	gtt	gac	aat	gca	tat	gca	aga	ggg	gtt	gtc	gtt	gtg	gcg	gct	768
Gln	Ala	Val	Asp	Asn	Ala	Tyr	Ala	Arg	Gly	Val	Val	Val	Val	Ala	Ala	
				245											255	
gct	ggg	aac	agc	gga	tct	tca	gga	aac	acg	aat	aca	atc	ggc	tat	cct	816
Ala	Gly	Asn	Ser	Gly	Ser	Ser	Gly	Asn	Thr	Asn	Thr	Ile	Gly	Tyr	Pro	
				260											270	
gcg	aaa	tac	gac	tct	gtc	atc	gca	gtt	ggc	gcg	gta	gac	cct	aac	agc	864

aaa ggt ctg atc aat gtc gaa gct gcc gct caa taa
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 370 375

1140

<210> 14
 <211> 379
 <212> PRT
 <213> Bacillus licheniformis

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Leu Val Phe Thr Met Ala Phe Ser Asp Ser Ala Ser Ala Ala Gln Pro
 20 25 30

Ala Lys Asn Val Glu Lys Asp Tyr Ile Val Gly Phe Lys Ser Gly Val
 35 40 45

Lys Thr Ala Ser Val Lys Lys Asp Ile Ile Lys Glu Ser Gly Gly Lys
 50 55 60

Val Asp Lys Gln Phe Arg Ile Ile Asn Ala Ala Lys Ala Lys Leu Asp
 65 70 75 80

Lys Glu Ala Leu Glu Glu Val Lys Asn Asp Pro Asp Val Ala Tyr Val
 85 90 95

Glu Glu Asp His Val Ala His Ala Leu Ala Gln Thr Val Pro Tyr Gly
 100 105 110

Ile Pro Leu Ile Lys Ala Asp Lys Val Gln Ala Gln Gly Tyr Lys Gly
 115 120 125

Ala Asn Val Lys Val Ala Val Leu Asp Thr Gly Ile Gln Ala Ser His
 130 135 140

Pro Asp Leu Asn Val Val Gly Gly Ala Ser Phe Val Ala Gly Glu Ala
 145 150 155 160

Tyr Asn Thr Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr Val
 165 170 175

Ala Ala Leu Asp Asn Thr Thr Gly Val Leu Gly Val Ala Pro Asn Val
 180 185 190

Ser Leu Tyr Ala Val Lys Val Leu Asn Ser Ser Gly Ser Gly Ser Tyr
 195 200 205

Ser Gly Ile Val Ser Gly Ile Glu Trp Ala Thr Thr Asn Gly Met Asp
 210 215 220

Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Thr Ala Met Lys
 225 230 235 240

Gln Ala Val Asp Asn Ala Tyr Ala Arg Gly Val Val Val Val Ala Ala
 245 250 255

1140379PRTBacillus licheniformis

Ala Gly Asn Ser Gly Ser Ser Gly Asn Thr Asn Thr Ile Gly Tyr Pro
 260 265 270

Ala Lys Tyr Asp Ser Val Ile Ala Val Gly Ala Val Asp Pro Asn Ser
 275 280 285

Asn Arg Ala Ser Phe Ser Ser Val Gly Ala Glu Leu Glu Val Met Ala
 290 295 300

Pro Gly Ala Gly Val Tyr Ser Thr Tyr Pro Thr Ser Thr Tyr Ala Thr
 305 310 315 320

Leu Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala
 325 330 335

Leu Ile Leu Ser Lys His Pro Asn Leu Ser Ala Ser Gln Val Arg Asn
 340 345 350

Arg Leu Ser Ser Thr Ala Thr Tyr Leu Gly Ser Ser Phe Tyr Tyr Gly
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Lys Gly Leu Ile Asn Val Glu Ala Ala Ala Gln
 370 375

<210> 15
 <211> 1146
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1146)

<400> 15
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 1 5 10 15

atc ttt acg atg gcg ttc agc aac atg tct gcg cag gct gcc gga aaa 96
 Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Ala Gly Lys
 20 25 30

agc agt aca gaa aag aaa tac att gtc gga ttt aaa cag aca atg agt 144
 Ser Ser Thr Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser
 35 40 45

gcc atg agt tcc gcc aag aaa aag gat gtt att tct gaa aaa ggc gga 192
 Ala Met Ser Ser Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly
 50 55 60

aag gtt caa aag caa ttt aag tat gtt aac gcg gcc gca gca aca ttg 240
 Lys Val Gln Lys Gln Phe Lys Tyr Val Asn Ala Ala Ala Thr Leu
 65 70 75 80

gat gaa aaa gct gta aaa gaa ttg aaa aaa gat ccg agc gtt gca tat 288
 Asp Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr
 85 90 95

gtg gaa gaa gat cat att gca cat gaa tat gcg caa tct gtt cct tat 336
 Val Glu Glu Asp His Ile Ala His Glu Tyr Ala Gln Ser Val Pro Tyr
 100 105 110

ggc att tct caa att aaa gcg ccg gct ctt cac tct caa ggc tac aca 384
 Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr
 115 120 125

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ggc tct aac gta aaa gta gct gtt atc gac agc gga att gac tct tct      432
Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser
130                               135                               140
cat cct gac tta aac gtc aga ggc gga gca agc ttc gta cct tct gaa      480
His Pro Asp Leu Asn Val Arg Gly Gly Ala Ser Phe Val Pro Ser Glu
145                               150                               155                               160
aca aac cca tac cag gac ggc agt tct cac ggt acg cat gta gcc ggt      528
Thr Asn Pro Tyr Gln Asp Gly Ser Ser His Gly Thr His Val Ala Gly
165                               170                               175
acg att gcc gct ctt aat aac tca atc ggt gtt ctg ggc gta gcg cca      576
Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro
180                               185                               190
agc gca tca tta tat gca gta aaa gtg ctt gat tca aca gga agc ggc      624
Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Asp Ser Thr Gly Ser Gly
195                               200                               205
caa tat agc tgg att att aac ggc att gag tgg gcc att tcc aac aat      672
Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ser Asn Asn
210                               215                               220
atg gat gtt atc aac atg agc ctt ggc gga cct act ggt tct aca gcg      720
Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Thr Gly Ser Thr Ala
225                               230                               235                               240
ctg aaa aca gtc gtt gac aaa gcc gtt tcc agc ggt atc gtc gtt gct      768
Leu Lys Thr Val Val Asp Lys Ala Val Ser Ser Gly Ile Val Val Ala
245                               250                               255
gcc gca gcc gga aac gaa ggt tca tcc gga agc aca agc aca gtc ggc      816
Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly Ser Thr Ser Thr Val Gly
260                               265                               270
tac cct gca aaa tat cct tct act att gca gta ggt gcg gta aac agc      864
Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala Val Gly Ala Val Asn Ser
275                               280                               285
agc aac caa aga gct tca ttc tcc agc gca ggt tct gag ctt gat gtg      912
Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala Gly Ser Glu Leu Asp Val
290                               295                               300
atg gct cct ggc gtg tcc atc caa agc aca ctt cct gga ggc act tac      960
Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Gly Thr Tyr
305                               310                               315                               320
ggc gct tat aac gga acg tcc atg gcg act cct cac gtt gcc cga gca      1008
Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Arg Ala
325                               330                               335
gca gcg tta att ctt tct aag cac ccg act tgg aca aac gcg caa gtc      1056
Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val
340                               345                               350
cgt gat cgt tta gaa agc act gca aca tat ctt gga aac tct ttc tac      1104
Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Asn Ser Phe Tyr
355                               360                               365
tat gga aaa ggg tta atc aac gta caa gca gct gca caa taa      1146
Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
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 <211> 381
 <212> PRT
 <213> Bacillus subtilis

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Ser	Ser	Thr	Glu	Lys	Lys	Tyr	Ile	Val	Gly	Phe	Lys	Gln	Thr	Met	Ser
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Ala	Met	Ser	Ser	Ala	Lys	Lys	Lys	Asp	Val	Ile	Ser	Glu	Lys	Gly	Gly
	50					55					60				
Lys	Val	Gln	Lys	Gln	Phe	Lys	Tyr	Val	Asn	Ala	Ala	Ala	Ala	Thr	Leu
65					70					75					80
Asp	Glu	Lys	Ala	Val	Lys	Glu	Leu	Lys	Lys	Asp	Pro	Ser	Val	Ala	Tyr
				85					90					95	
Val	Glu	Glu	Asp	His	Ile	Ala	His	Glu	Tyr	Ala	Gln	Ser	Val	Pro	Tyr
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Gly	Ile	Ser	Gln	Ile	Lys	Ala	Pro	Ala	Leu	His	Ser	Gln	Gly	Tyr	Thr
		115					120					125			
Gly	Ser	Asn	Val	Lys	Val	Ala	Val	Ile	Asp	Ser	Gly	Ile	Asp	Ser	Ser
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His	Pro	Asp	Leu	Asn	Val	Arg	Gly	Gly	Ala	Ser	Phe	Val	Pro	Ser	Glu
145				150					155						160
Thr	Asn	Pro	Tyr	Gln	Asp	Gly	Ser	Ser	His	Gly	Thr	His	Val	Ala	Gly
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Thr	Ile	Ala	Ala	Leu	Asn	Asn	Ser	Ile	Gly	Val	Leu	Gly	Val	Ala	Pro
			180					185					190		
Ser	Ala	Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	Asp	Ser	Thr	Gly	Ser	Gly
		195					200					205			
Gln	Tyr	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	Trp	Ala	Ile	Ser	Asn	Asn
	210					215					220				
Met	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro	Thr	Gly	Ser	Thr	Ala
225				230						235					240
Leu	Lys	Thr	Val	Val	Asp	Lys	Ala	Val	Ser	Ser	Gly	Ile	Val	Val	Ala
				245					250					255	
Ala	Ala	Ala	Gly	Asn	Glu	Gly	Ser	Ser	Gly	Ser	Thr	Ser	Thr	Val	Gly
			260					265					270		
Tyr	Pro	Ala	Lys	Tyr	Pro	Ser	Thr	Ile	Ala	Val	Gly	Ala	Val	Asn	Ser
		275					280					285			
Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	Ala	Gly	Ser	Glu	Leu	Asp	Val
		290				295					300				
Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	Leu	Pro	Gly	Gly	Thr	Tyr
305					310					315					320

Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Arg Ala
 325 330 335

Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val
 340 345 350

Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Asn Ser Phe Tyr
 355 360 365

Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
 370 375 380

<210> 17
 <211> 32
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 17
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<210> 18
 <211> 34
 <212> DNA
 <213> Artificial

<220>
 <223> Description of artificial sequence: Primer

<400> 18
 ggtagatctc ttctgctgctc ttcaagaatt ccgc 34

<210> 19
 <211> 441
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(441)

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 aaa gta gcc gtc ctg gat aca gga atc caa gct tct cat ccg gac ttg 96
 Lys Val Ala Val Leu Asp Thr Gly Ile Gln Ala Ser His Pro Asp Leu
 20 25 30
 aac gta gtc ggc gga gca agc ttt gtg gct ggc gaa gct tat aac acc 144
 Asn Val Val Gly Gly Ala Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr
 35 40 45
 gac ggc aac gga cac ggc gca cat gtt gcc ggt aca gta gct gcg ctt 192
 Asp Gly Asn Gly His Gly Ala His Val Ala Gly Thr Val Ala Ala Leu
 50 55 60

gac aat aca acg ggt gta tta ggc gtt gcg cca agc gta tcc ttg tac	240
Asp Asn Thr Thr Gly Val Leu Gly Val Ala Pro Ser Val Ser Leu Tyr	
65 70 75 80	
gcg gtt aaa gta ctg aat tca agc gga agc gga tca tac agc ggc att	288
Ala Val Lys Val Leu Asn Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile	
85 90 95	
gta agc gga atc gag tgg gcg aca aca aac ggc atg gat gtt atc aat	336
Val Ser Gly Ile Glu Trp Ala Thr Thr Asn Gly Met Asp Val Ile Asn	
100 105 110	
atg agc ctt ggg gga gca tca ggc tcg aca gcg atg aaa cag gca gtc	384
Met Ser Leu Gly Gly Ala Ser Gly Ser Thr Ala Met Lys Gln Ala Val	
115 120 125	
gac aat gca tat gca aaa ggg gtt gtc gtt gta gct gca gca ggg aac	432
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Ser Gly Ser	
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<210> 20
 <211> 147
 <212> PRT
 <213> Bacillus subtilis

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Lys Val Ala Val Leu Asp Thr Gly Ile Gln Ala Ser His Pro Asp Leu
20 25 30
Asn Val Val Gly Gly Ala Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr
35 40 45
Asp Gly Asn Gly His Gly Ala His Val Ala Gly Thr Val Ala Ala Leu
50 55 60
Asp Asn Thr Thr Gly Val Leu Gly Val Ala Pro Ser Val Ser Leu Tyr
65 70 75 80
Ala Val Lys Val Leu Asn Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile
85 90 95
Val Ser Gly Ile Glu Trp Ala Thr Thr Asn Gly Met Asp Val Ile Asn
100 105 110
Met Ser Leu Gly Gly Ala Ser Gly Ser Thr Ala Met Lys Gln Ala Val
115 120 125
Asp Asn Ala Tyr Ala Lys Gly Val Val Val Val Ala Ala Ala Gly Asn
130 135 140
Ser Gly Ser
145

<210> 21
 <211> 576
 <212> DNA

